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(54) METHOD FOR IDENTIFYING AND SPECIFICALLY DETECTING SLOWLY GROWING MYCOBACTERIA USING CHARACTERISTIC BASE SEQUENCE PRESENT IN DNA GYRASE GENE

(57)Abstract:

PROBLEM TO BE SOLVED: To allow accurately identifying/detecting slowly growing mycobacteria which can not be easily detected so far.

SOLUTION: This is a method for identifying and detecting slowly growing mycobacteria utilizing a characteristic base sequence present in *gyrB* gene.

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(54) 【発明の名称】 DNAジャイレース遺伝子中に存在する特徴的な塩基配列を用いた遅発育性マイコバクテリアの
同定法及び特異的検出法

(57) 【要約】

【解決手段】 gyrB遺伝子中に存在する特徴的な塩基配列を利用して遅発育性マイコバクテリアの同定及び検出を行う方法。

【効果】 従来、同定及び検出が困難であった遅発育性マイコバクテリアについても正確に同定・検出を行うことが可能になる。

【特許請求の範囲】

【請求項1】 遅発性マイコバクテリアのDNAジャイレースβサブユニットをコードするDNA中の配列番号7～22に対応する領域を増幅し、その増幅断片の塩基配列を配列番号7～22記載の塩基配列と比較し、各配列からの遺伝学的距離を求め、その遺伝学的距離により前記遅発性マイコバクテリアの同定を行うことを特徴とする遅発性マイコバクテリアの同定方法。

【請求項2】 配列番号4記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・カンサシイを検出することを特徴とするマイコバクテリウム・カンサシイの検出方法。

【請求項3】 配列番号4記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを含むことを特徴とするマイコバクテリウム・カンサシイの検出用キット。

【請求項4】 配列番号6記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・ガストリを検出することを特徴とするマイコバクテリウム・ガストリの検出方法。

【請求項5】 配列番号6記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを含むことを特徴とするマイコバクテリウム・ガストリの検出用キット。

【発明の詳細な説明】

【0001】

【発明の属する技術分野】 本発明は、結核並びに非結核性抗酸菌の原因菌として多くの症例数のある遅発性マイコバクテリアのDNAジャイレースβサブユニットをコードするDNA(以下、「*gyrB*遺伝子」という)の塩基配列を利用した同定・検出法に関するものである。本発明の同定・検出法は、各種産業分野において有用である。

【0002】

【従来の技術】 ヒトに結核並びに結核類似症を引き起こす抗酸菌種は遅発性マイコバクテリアの属する種が複数知られている。その中でも臨床例としてはマイコバクテリウム・ツベルクローシス・コンプレックス (*Mycobacterium tuberculosis complex*)、マイコバクテリウム・アビウム・コンプレックス (*Mycobacterium avium complex*)、マイコバクテリウム・カンサシイ (*Mycobacterium kansasii*) がその大半を占めている。最近では後天性免疫不全症候群 (AIDS) 患者等においてはこれらの

細菌が全身播種性感染を引き起こし、AIDS患者の予後の重大な問題となっている。

【0003】 従来これらの菌種の同定・検出は、培養に基づく生理生化学的な方法によって行われていた。例えば、遅発性マイコバクテリアの中には、1) 光を照射した後に暗所で培養した場合にのみ黄色に発色するグループ (光発色菌)、2) 光を照射せずに培養しても発色するグループ (暗発色菌)、3) 光を照射しても発色しないグループ (非発色菌) の3グループが存在するので、この発色の違いを利用して同定・検出を行うことが行われてきた。また、培養した細菌がカタラーゼ生産を行うかどうか、ウレアーゼ活性、トウイーン加水分解活性あるいは硝酸塩還元活性を示すかどうか、などにより同定・検出を行う方法も知られていた。

【0004】 しかし、これらの検査は純粋培養を必要とする上、比較の対象となる表現型は変化しやすく、判定が主観的になりがちであった。その結果、時間がかかる上に、正確な種の判定は極めて困難であった。この様な問題点を解決するために、近年になってポリメラーゼ連鎖反応 (以下、「PCR」という) 法などを用いて遺伝子の特定の塩基配列の有無を判定する同定・検出の方法が考案され利用されるようになった。PCR法は、培養を必要とせず迅速かつ客観的な判定を得るという点で、遅発性マイコバクテリアの同定・検出に適している。

【0005】 その際、用いられる遺伝子は多くの場合、rRNA遺伝子である。T. Rogallら (1990. J. Gen. Microbiol. 136, 1915-1920) は、16S rRNA配列を用いたPCRに基づくマイコバクテリア種の同定法を提案した。しかしながら、これらのプライマーは、異なった表現型特性を示すマイコバクテリウム・ガストリ (*Mycobacterium gastri*) とマイコバクテリウム・カンサシイを区別できなかった。一方B. Boddinghausら (1990. J. Clin. Microbiol. 28: 1751-1759) は、ヒト型結核菌グループや鳥型結核菌-バラ結核菌およびマイコバクテリウム・イントラセルラーレ (*Mycobacterium intracellulare*) グループに特異的である16S rRNA配列に由来するオリゴヌクレオチドを報告した。このオリゴヌクレオチドを用いても種のレベルでの同定を行う為に必要な解像度は得られなかった。これらのrRNA遺伝子配列を利用した同定法は、現在商品化され、日本ロッシュから「アンブリコア・マイコバクテリウム」という商品名の遺伝子診断キットとして販売されている。その他にも、東洋紡社 (特開平10-323189号公報) やベクトン・ディッキンソン・アンド・カンパニー (特開平10-057098号公報) からrRNA配列を利用した検出あるいは同定法が開示されている。上に記したような二つの種を判別できない問題を解決するために、16S rRNAと23S rRNAの間の領域の配列を用いた同定・検出法がA. Rothらによって提案されている (1998. J. Clin. Microbiol. 36: 139-147)。しかし、16S rRNAと23S rRNAの間の領域は約200塩基対しかなく、

このような短い配列により精度の高い分子系統学的解析は困難で二菌種のどちらの配列とも一致しない中間的な配列を持つ新規株が現れた場合、どちらにより近縁かといった判断を下すことができない一方、シュードモナス (*Pseudomonas*) 属、アシネトバクター (*Acinetobacter*) 属を始め、多くの細菌で、進化速度の速いタンパク質をコードする遺伝子、なかでも *gyrB* 遺伝子の1200塩基対の配列を用いることによって、より詳細で正確な分類・同定ができることが示された (Yamamoto, S. and S. Harayama. 1995. Appl. Environ. Microbiol. 61: 1104-1109. Yamamoto, S. and S. Harayama. 1996. Int. J. Syst. Bacteriol. 46: 506-511. Harayama, S. and S. Yamamoto. 1996. p250-258 In Molecular Biology of *Pseudomonas* T. Nakazawa, K. Fukuda, D. Haas, S. Silver (eds) ASM press, Washington, D.C., 山本 敏、原山重明、化学と生物 1996 第34巻 第3号 p. 149-151., 山本 敏、原山重明、農芸化学会誌 1997 第71巻 第9号 p. 894-897.)。

【0006】*gyrB* 遺伝子以外のタンパク質をコードする遺伝子を用いて遅発育性マイコバクテリアの同定を行う試みは行われている。例えば、C. T. Shivannvarらはスーパーオキシド・ディスムターゼ遺伝子を利用して遅発育性のマイコバクテリアの系統関係と抗原性の関係を論じ (1994. J. Clin. Microbiol. 32: 2801-2812)、D. S. Swansonらは65 kD 熱ショックタンパク質遺伝子を用いて鳥型結核菌-パラ結核菌およびマイコバクテリウム・イントラセルラーレググループの詳細な分類を試みた (1997. Int. J. Syst. Bacteriol. 47: 414-419)。米国アボット・ラボラトリーズは特表平10-500567 (国際公開番号W095/31571) としてrRNA遺伝子以外にもマイコバクテリウム・ツベルクロシスのタンパク質抗原8をコードする遺伝子や、マイコバクテリウム・ツベルクロシスの65 kD熱ショックタンパク質、10kD熱ショックタンパク質等の遺伝子配列並びに挿入配列IS987やIS6110の関連する配列を用いた検出法を開示している。他にもベクトン・ディッキンソン・アンド・カンパニーはマイコバクテリウム・パラツベルクロシスの70kD熱ショックタンパク質をコードする遺伝子に由来する検出・同定するプローブを特開平06-319560として開示している。しかしながら、これらの遺伝子のうち、分子系統学的に得られるデータと従来の分類学的な手法による種の同定と比較した場合、矛盾が認められないことが示されているのは *gyrB* 遺伝子のみであり (Yamamoto and Harayama 1998. Int. J. Syst. Bacteriol. 48: 813-819. Yamamoto et al. 1999. Int. J. Syst. Bacteriol. 49: 87-95. Suzuki et al. 1999. Int. J. Syst. Bacteriol. in press, Kasai et al. 1999. Int. J. Syst. Bacteriol. in press)、新規に分離された株についても正確な分子系統学的な位置を決定でき、更に他の遺伝子では区別できなかった近縁種の区別できることなどから他の遺

伝子を用いた方法より有効な方法である。

【0007】

【発明が解決しようとする課題】*gyrB* 遺伝子を用いた細菌の同定・検出法については、既に本出願人により出願されている (特開平11-169175号公報)。しかし、この公報中では、遅発育性マイコバクテリアの同定・検出を行うに当たって *gyrB* 遺伝子中のどの領域を利用すればよいかについては明らかにされていなかった。

【0008】遅発育性マイコバクテリアには結核などの重要な疾病の原因細菌が含まれるため、この細菌群を正確に同定・検出するための方法が強く望まれている。一方、遅発育性マイコバクテリアは、生育速度が通常の細菌よりも遅いため、細菌の培養を必須とする生理生化学的方法では同定・検出が難しい。本発明は、このような技術的背景の下になされたものであり、*gyrB* 遺伝子を利用した遅発育性マイコバクテリアの同定・検出方法を提供することにある。

【0009】

【課題を解決するための手段】本発明者らは遅発育性マイコバクテリアの標準株の *gyrB* 遺伝子配列を決定した。それらの配列に対して臨床から分離された株の分類学的な位置づけを行った。分類学的位置づけが矛盾のないことを、細菌の種の同定の標準的方法であるDNA-DNA 交雑法によって確認した。

【0010】また、遺伝子配列を利用した細菌の検出法として最も一般的に用いられる16S rRNA遺伝子の配列では区別できない非結核性抗酸菌マイコバクテリウム・ガストリとマイコバクテリウム・カンサシイの標準株のDNAから *gyrB* 断片をPCR法によって増幅し塩基配列を決定した。得られた配列を比較したところ、両株の16S rRNA遺伝子配列は同一であるにも関わらず、両株の *gyrB* 遺伝子配列1257塩基配列中66箇所が異なっていることを見出した (図1)。それらの配列の違いを利用して両菌種それぞれに特異的なPCR増幅を可能にしたプライマーを設計した。

【0011】本発明は、以上の知見により完成されたものである。即ち、本発明は、遅発育性マイコバクテリアの *gyrB* 中の配列番号7~22に対応する領域を増幅し、その増幅断片の塩基配列を配列番号7~22記載の塩基配列と比較し、各配列からの遺伝学的距離を求め、その遺伝学的距離により前記遅発育性マイコバクテリアの同定を行うことを特徴とする遅発育性マイコバクテリアの同定方法である。

【0012】また、本発明は、配列番号4記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・カンサシイを検出することを特徴とするマイコバクテリウム・カンサシイの検出方法、及び前記オリゴヌク

レオチドを含むマイコバクテリウム・カンサシイの検出用キットである。

【0013】更に、本発明は、配列番号6記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・ガストリを検出することを特徴とするマイコバクテリウム・ガストリの検出方法、及び前記オリゴヌクレオチドを含むマイコバクテリウム・ガストリの検出用キットである。

【0014】

【発明の実施の形態】以下、本発明を詳細に説明する。

(1) 同定方法

本発明の遅発育性マイコバクテリアの同定方法は、遅発育性マイコバクテリアのgyrB中の配列番号7～22に対*

* 応する領域をPCRにより増幅し、その増幅断片の塩基配列を配列番号7～22記載の塩基配列と比較し、各配列からの遺伝学的距離を求め、その遺伝学的距離により前記遅発育性マイコバクテリアの同定を行うことを特徴とする。

【0015】本発明において同定とは、分子系統学的手法等によって細菌の分類学的な位置を定めることをいう。gyrB中の配列番号7～22に対応する領域を増幅するためのプライマーとしては、例えば、配列番号39及び配列番号40により表されるプライマーを例示することができるが、これらに限定されるわけではない。配列番号7～22記載の塩基配列と、対応するアミノ酸配列及び由来とする微生物の名称との関係は、下表の通りである。

【0016】

【表1】

塩基配列	アミノ酸配列	由来とする微生物の名称
配列番号7	配列番号23	マイコバクテリウム・シミエ
配列番号8	配列番号24	マイコバクテリウム・ボビス
配列番号9	配列番号25	マイコバクテリウム・スツルガイ
配列番号10	配列番号26	マイコバクテリウム・マルモエンセ
配列番号11	配列番号27	マイコバクテリウム・イントラセルラーレ
配列番号12	配列番号28	マイコバクテリウム・アビウム
配列番号13	配列番号29	マイコバクテリウム・ゴールドナエ
配列番号14	配列番号30	アミコバクテリウム・アフリカヌム
配列番号15	配列番号31	マイコバクテリウム・ツベルクロシス
配列番号16	配列番号32	マイコバクテリウム・ガストリ
配列番号17	配列番号33	マイコバクテリウム・マリヌム
配列番号18	配列番号34	マイコバクテリウム・ミクロティ
配列番号19	配列番号35	マイコバクテリウム・アジアティカム
配列番号20	配列番号36	マイコバクテリウム・スクロファアラセウム
配列番号21	配列番号37	マイコバクテリウム・ブランデリ
配列番号22	配列番号38	マイコバクテリウム・パラツベルクロシス

【0017】遺伝学的距離は、例えば、Phylip プログラムの説明書にあるFelsenstein記載の方法に従って求めることができる (Felsenstein, J. 1993. PHYLIP(PhylogenyInference Package) version 3.5c. Distributed by the author, Department of Genetics, University of Washington, Seattle, U.S.A.)。

【0018】(2) 特異的検出

本発明のマイコバクテリウム・カンサシイの検出方法は、配列番号4記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることを特徴とするものである。また、本発明のマイコバクテリウム・カンサシイの検出用キットは、前記オリゴヌクレオチドを含むことを特徴とするものである。

【0019】本発明のマイコバクテリウム・ガストリの検出方法は、配列番号6記載のアミノ酸配列の一部若し

くは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることを特徴とするものである。また、本発明のマイコバクテリウム・ガストリの検出用キットは、前記オリゴヌクレオチドを含むことを特徴とするものである。

【0020】ここで、「プライマー又はプローブとして実質的に機能する」とは、特異的なアニール又はハイブリダイズが可能な程度の長さを有するという意味であり、検出対象とするDNAとアニール又はハイブリダイズする配列を有しているが、その長さが短いため非特異的なアニール又はハイブリダイゼーションを頻繁に起こし、特異的な検出に使用できないようなオリゴヌクレオチドを排除する趣旨である。

【0021】マイコバクテリウム・カンサシイの検出に利用できるオリゴヌクレオチドとしては、配列番号3により表されるオリゴヌクレオチドを例示でき、マイコバ

クテリウム・ガストリの検出に利用できるオリゴヌクレオチドとしては、配列番号5により表されるオリゴヌクレオチドを例示できるが、これらに限定されるわけではない。

【0022】検出の対象とするDNAの調製、プライマーの作製及びそれを用いたPCR、プローブの調製及びそれを用いたハイブリダイゼーションは、常法に従って行うことができ、特別な方法を用いる必要はない。

【0023】なお、PCRに使用するプライマーは、両方が特異的にアニールするものである必要は必ずしもなく、一方は非特異的にアニールするものであってもよい。このような非特異的にアニールするプライマーの一例としては、配列番号1記載の塩基配列により表されるプライマーを挙げることができる。

【0024】

【実施例】【実施例1】配列番号39及び配列番号40記載の塩基配列により表されるオリゴヌクレオチドを利用して、臨床患者より分離された抗酸菌株8菌株（KPM 2201T、KPM 2202、KPM 2203、KPM 2013、KPM 2014、KPM 1988-5、KPM 2209、KPM 2212）のgyrB遺伝子配列を決定した。得られたgyrB配列と遅発育性マイコバクテリア同定用gyrB配列セット（配列番号7-38）を利用して分子系統学的解析により系統関係を推定した。分子系統学的解析は、分子系統学的解析用汎用プログラムClustal W (Thompson, J. D., D. G. Higgins, and T. J. Gibson. 1994. Clustal W: improving the sensitivity of progressive multiple sequence alignment through sequence weight

*ghting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Res. 22: 4673-4680.)あるいはPhylip (Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c. Distributed by the author, Department of Genetics, University of Washington, Seattle, U.S.A.)等を用い、両プログラムの使用説明書に従い、以下のように行った。配列番号39及び配列番号40記載の塩基配列により表されるオリゴヌクレオチドを使用して得られたgyrB配列と配列番号7-38の遅発育性マイコバクテリア同定用gyrB配列セットをClustal Wプログラムにより多重整列ファイルを作成する。多重整列させる際に用いるパラメーターの一例は"Gap Open Penalty: 15.00; Gap Extension Penalty: 6.66; DNA weight matrix: IUB; DNA transition weight: 0.5"である。得られた多重整列はアミノ酸配列から得られる多重整列ファイルと比較し、問題のある箇所は訂正する。次に、多重整列ファイルをもとに各配列間の遺伝学的距離を算出する。算出には、Phylipのdnadistプログラムを使用する。算出はKimura 2-parameter modelに従って行う。得られた遺伝学的距離から近隣結合法により系統樹を作成する。系統樹の分岐の確かさはbootstrap確率を計算すること等により検定する。一方、上記8菌株を16S rRNA遺伝子を利用した手法及び生化学的手法によっても同定した。以上の結果を表2に示す。

【0025】

【表2】

株名	生化学的試験	16S rRNA 遺伝子	DNA 相同性試験
KPM 2201T	<u>M. gordonae</u>	<u>M. gordonae</u>	<u>M. gordonae</u>
KPM 2202	<u>M. gastori</u>	<u>M. gordonae</u>	<u>M. gordonae</u>
KPM 2203	<u>M. gastori</u>	<u>M. gordonae</u>	<u>M. gordonae</u>
KPM 2013	<u>M. scrofulcerum</u>	<u>M. gordonae</u>	新種
KPM 2014	<u>M. scrofulcerum</u>	<u>M. gordonae</u>	新種
KPM 1988-5	<u>M. scrofulcerum</u>	<u>M. gordonae</u>	新種
KPM 2209	<u>M. scrofulcerum</u>	<u>M. gordonae</u>	新種
KPM 2212	データなし	<u>M. gordonae</u>	新種

【0026】表が示すように、上記8菌株のうち、KPM 2201T、KPM 2202、KPM 2203の3菌株は、マイコバクテリア・ゴールドナエに属するものと同定されたが、残りのKPM 2013、KPM 2014、KPM 1988-5、KPM 2209、KPM 2212の5菌株は、マイコバクテリア・ゴールドナエと近縁ではあるが別種（新種）であることが示唆された（図3）。この結果を、検証するためにDNA-DNA交雑試験（Ezaki, T., Hashimoto, Y., Takeuchi, T., Yamamoto, H., Shu-Lin Liu, Matsui, K., & Yabuuchi, E (1988). J. Clin. Microbiol. 26, 1708-1713. Ezaki, T., Hashimoto, Y., Takeuchi & Yabuuchi, E (1989). Int. J. Syst. Bacteriol. 39, 224-229)を行ったところ新種であることが支持された。この結果は、遅発育性マイコバクテリア同定用gyrB配列セットが既知の株のみならず新

種の株に対しても信頼性の高い結果を与えることを示している。

【0027】【実施例2】マイコバクテリア・カンサシとマイコバクテリア・ガストリのgyrB遺伝子の塩基配列を比較し（図1）、マイコバクテリア・カンサシのgyrB遺伝子に特異的にアニールするプライマー（配列番号3）とマイコバクテリア・ガストリに特異的にアニールするプライマー（配列番号5）を作製した。また、両菌種のgyrB遺伝子にアニールするプライマー（配列番号1）も作製した。

【0028】これらのプライマーを用いて、臨床患者より単離された株 KPM 1004, KPM 1007, KPM KY256, KPM KY761, KPM KY768, KPM 1988-1, KPM 3502, KPM 3503の菌体破砕液についてPCRを行った。PCR法による増幅条件

は次のとおりである。

【0029】

95 °C 10分 1サイクル
95 °C 1分、68 °C 1分30秒 30サイクル
72 °C 10分 1サイクル
プライマー濃度 各1 μM
dNTP 各 100 μM

Ampli Taq GOLD[®]及び添付のPCR buffer Iを使用(米国 Perkin Elmer社)

【0030】増幅されたDNA断片を電気泳動法により解 10 【0031】
析したところ、KPM 1004, KPM 1007, KPM KY256, KPM K* 【表3】

	<u>M. kansasii</u>	<u>M. gastri</u>
配列番号 1	増幅可。	増幅不可。
配列番号 3		
配列番号 1	増幅不可。	増幅可。
配列番号 5		

【0032】

【発明の効果】本発明は、これまで同定することが困難であった遅発育性マイコバクテリアの分類同定を正確に 20 行うことを実現するものである。また非結核性抗酸菌のうち16S rRNA 遺伝子配列に基づく同定法では鑑別が困 ※

※難であった菌種、例えばマイコバクテリウム・カンサシイとマイコバクテリウム・ガストリイの迅速同定が可能となる。

【0033】

【配列表】

SEQUENCE LISTING

<10> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD

<20> DNA GYRESU IDENSHICHI NI SONZAISURU TOKUCHYOUTEKINA ENKIHAIRETSU
WO MOCHIITA CHIHATSUKUSEI MAIKOBAKUTERIA NO DOUTEIHOU OYOBI TOKUITEKI K
ENSHUTSUHOU

<30> P99-0373

<60> 40

<70> PatentIn Ver. 2.0

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<212> DNA

<213> Artificial Sequence

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<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 2

Gly Val Ser Val Val Asn

<210> 3

<211> 20

<212> DNA

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<400> 3

gac ctt gtg cgg ggc ggc gg

<210> 4

<211> 6

11

12

<212> PRT

<213> Artificial Sequence

<400> 4

Ala Ala Pro His Lys Val

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<400> 5

cac ctt gtg ggg ggc ggt ga

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 6

Thr Ala Pro His Lys Val

<210> 7

<211> 1263

<212> DNA

<213> Mycobacterium simiae

<220>

<221> CDS

<222> (1)..(1263)

<400> 7

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1 5 10 15	
gtg tcg gtg gtc aac gcc ctg tcc acc cgc ctg gaa gtc aac gtc aag	96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys	
20 25 30	
cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc	144
Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly	
35 40 45	
acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg	192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg	
50 55 60	
ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag	240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu	
65 70 75 80	
acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg	288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat	336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	
100 105 110	
gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag	384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln	
115 120 125	
gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac	432
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His	

13	14
130	140
tac ccg ggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa 480	
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145	150
aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg 528	
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly	
165	170
cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg 576	
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180	185
gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac 624	
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195	200
gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc 672	
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210	215
aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac 720	
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225	230
gac atc cga gaa ggg ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag 768	
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	
245	250
ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc 816	
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val	
260	265
aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc 864	
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe	
275	280
gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg 912	
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser	
290	295
tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg 960	
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg	
305	310
cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat 1008	
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp	
325	330
tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt 1056	
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly	
340	345
gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag 1104	
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln	
355	360
gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc 1152	
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg	
370	375
atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg 1200	
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala	
385	390
ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac 1248	

15
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 cac aag atc gtg ttg 1263
 His Lys Ile Val Leu
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 gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac 96
 Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 ggg tac gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg ggc ctc 144
 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 aag caa ggg gcg ccg acc aag aag acg ggg tca acg gta cgg ttc tgg 192
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc 240
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc 288
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg 336
 Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc 384
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
 115 120 125
 gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg 432
 Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
 130 135 140
 ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg 480
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag 528
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac 576
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag 624

17
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
 195 200 205
 ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac 672
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc 720
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag 768
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
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 260 265 270
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 275 280 285
 aac ccc acc gac tcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg 912
 Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag 960
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt 1008
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg 1056
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
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 355 360 365
 ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac 1152
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg gcc 1200
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag 1248
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gtg tcg gtg gtg aac gcg ctg tcg acc cgg ctc gag gtc gac atc aag 96	
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys	
20 25 30	
cgt gac ggc cac aag tgg tcg cag ttc tac aac aag gcc gtg ccg ggc 144	
Arg Asp Gly His Lys Trp Ser Gln Phe Tyr Asn Lys Ala Val Pro Gly	
35 40 45	
acg ctc aaa cag ggt gaa gcc act aag aaa acc gga acg aca att aag 192	
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg	
50 55 60	
ttc tgg gcc gac ccg gac atc ttc gag acc acc gaa tac gac ttc gag 240	
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu	
65 70 75 80	
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Thr Ile Asn Leu Thr Asp Glu Arg Val Ala Gln Asp Glu Val Val Asp	
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Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys	
115 120 125	
ggc gcc gaa tcc aaa ggg ccg cat aag gtt aag cac cgc act ttc cat 432	
Ala Ala Glu Ser Lys Gly Pro His Lys Val Lys His Arg Thr Phe His	
130 135 140	
tac ccc ggc ggg ctg atc gac ttc gtc aag cac atc aac cgg acc aag 480	
Tyr Pro Gly Gly Leu Ile Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
agc ccg atc cag cag agt gtc gtc gcc ttc gac ggc aag ggt gaa ggg 528	
Ser Pro Ile Gln Gln Ser Val Val Ala Phe Asp Gly Lys Gly Glu Gly	
165 170 175	
cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tat tcg gag tcg 576	
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	
gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac 624	
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gaa gaa ggg ttc cgc agc gca ctg aca tcg gtg gtg aac aag tac gcc 672	
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaa gac aag aag ctg ctc aag gag aag gac gcc aac ctc acc ggc gac 720	
Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Ala Asn Leu Thr Gly Asp	
225 230 235 240	
gac att cgc gag ggc ctg gcc gcg gtc atc tcg gtg aaa gtt gcc gaa 768	
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	
245 250 255	
ccg cag ttc gag ggc cag acc aag acc aaa ctg ggt aac acc gag gtc 816	

21

22

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 aag tcg ttc gta cag aag gtc tgc aac gaa cag ctg acc cac tgg ttc 864
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 gag gcc aac ccg tcg gaa gcc aaa acc gtc gtg aac aag gcg gtc tcg 912
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 tcg gca cag gcg cgt atc gcc gcc cgc aag gca cga gag ttg gtg cgt 960
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 cgc aag agc gct acc gat ctc ggt ggg ctg ccc gcc aag ctg gcc gac 1008
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 tgc cgc tcc acc gat ccg cgc aag tcg gaa ttg tat gtg gtg gaa ggg 1056
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 gac tcg gcc gcc gcc tcc gcc aag agc gcc cgc gac tcg atg ttt cag 1104
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 gcg ata ctt ccg ttg cgc gcc aag atc atc aac gtc gag aag gcc cgc 1152
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 atc gac cgg gtg ctg aag aac acc gaa gtc cag gcg atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 ctg ggt acc gga att cac gac gag ttc gac ctc gcc aaa ctg cgc tac 1248
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ala Lys Leu Arg Tyr
 405 410 415
 cac aag atc gtg ctg 1263
 His Lys Ile Val Leu
 420
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 Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 gtg tcg gtg gtc aac gcg ttg tcg acc cgg ctc gag gtg gat gtc gcc 96
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Val Ala
 20 25 30
 cgc gac gcc tac atg tgg tca cag ttc tac gat cac gcc gag ccg gga 144
 Arg Asp Gly Tyr Met Trp Ser Gln Phe Tyr Asp His Ala Glu Pro Gly
 35 40 45
 acc ctc aaa cag gcc gag gcc acc aag acg acg gga acc acc atc agg 192

23	24
Thr Leu Lys Gln Gly Glu Ala Thr Lys Thr Thr Gly Thr Thr Ile Arg	
50 55 60	
ttc tgg gcc gat ccc gac atc ttc gag acc acc gag tac gac ttc gag	240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu	
65 70 75 80	
acg gtg gcg cgc cga ctg cag gaa atg gcg ttc ctg aac aag ggt ttg	288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acg atc aac ctc acc gac gag cgg gtc agt gaa gag gag gtc gtc gac	336
Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Glu Glu Glu Val Val Asp	
100 105 110	
gat gtc gtc agc gac acc gcc gag gca ccc aag tcc gcc gta gaa aaa	384
Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Val Glu Lys	
115 120 125	
gcg gcc gaa tcg act ggc cca cac aag gtt aag cac cgc acg ttc cac	432
Ala Ala Glu Ser Thr Gly Pro His Lys Val Lys His Arg Thr Phe His	
130 135 140	
tac ccg ggc ggc ttg gtg gac ttc gtc aag cac atc aat cgg acc aag	480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
aac ccg att cac aac agc atc gtg gat ttc tcc gcc aag gga ccg gcc	528
Asn Pro Ile His Asn Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly	
165 170 175	
cac gag gtc gaa atc gcg atg cag tgg aat gcc gcc tac tcg gag tcg	576
His Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser	
180 185 190	
gtg cac acc ttc gcc aac acc atc aac acc cac gag gcc gcc acc cac	624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gaa gag gcc ttc cgc agc gcg ttg acg tcg gtg gtc aac aaa tac gcc	672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaq gac cgc aaa ctc ctg aag gac aaa gac ccc aac ctc acc gcc gac	720
Lys Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225 230 235 240	
gac atc cgg gaa gcc ctg gca gcg gtc att tcc gtc aag gtc agc gaa	768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu	
245 250 255	
ccg caa ttc gag gcc cag acc aaa acc aag ctg gcc aac acc gag gtc	816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val	
260 265 270	
aaq tcg ttc gtg cag aag gtc tgc aac gaa cag ctc acg cac tgg ttc	864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe	
275 280 285	
gaa gcc aac ccg gcg gat gcc aaa act gtt gta aac aag gcg gtt tcg	912
Glu Ala Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser	
290 295 300	
tcg gcc cag gcc cga atc gca gcg cgc aag gcg cga gaa ctg gtg cgc	960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg	
305 310 315 320	

25		26
cgc aag agc gcc acc gac ctc ggt ggg ctg ccg ggt aag ctc gca gac	1008	
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp		
325 330 335		
tgc cgc tcc acc gac ccg cga aag tcg gaa ctg tat gtg gtg gag ggt	1056	
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly		
340 345 350		
gac tcg gcc ggc gcc tcg gcc aag agc ggc cgc gac tcg atg ttc cag	1104	
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln		
355 360 365		
gcg atc ctc ccg ctg cgt ggc aag atc atc aac gtc gag aag gcg cgc	1152	
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg		
370 375 380		
atc gac cgg gtg ctg aag aac acc gaa gtt cag gcg atc atc acc gcg	1200	
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala		
385 390 395 400		
ctg ggc acg ggg att cac gac gag ttc gac atc acc aag ctc ccg tac	1248	
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr		
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cac aag atc gtg ctg	1263	
His Lys Ile Val Leu		
420		
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Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly		
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gtc tcg gtg gtc aac gcg ctg tcg acc ccg ctc gag gtg gac atc gcc	96	
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Ala		
20 25 30		
cgc gat ggc tac gaa tgg tcg cag ttc tac gac cac gcc gta ccc gga	144	
Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp His Ala Val Pro Gly		
35 40 45		
acg ctc aaa cag ggt gag gcc acc aag ccg acg ggc acc acg atc agg	192	
Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg		
50 55 60		
ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gag	240	
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu		
65 70 75 80		
acg gtg gcg cgc ccg ctg cag gaa atg gcg ttc ctc aac aag ggg ttg	288	
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu		
85 90 95		
acc atc aac ctc acc gac gag ccg gtg agc aac gag gag gtc gtc gac	336	
Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Asn Glu Glu Val Val Asp		
100 105 110		

27	28
gag gtc gtc agc gat acc gcc gac gca ccc aag tcg gcc cag gaa aag 384	
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys	
115 120 125	
gcg gcg gaa tcg act gcg cca cat aag gtt aag cac cgc acc ttc cac 432	
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His	
130 135 140	
tac ccc gcc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag 480	
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
agc ccg atc cag cag agc atc atc gac ttc gac gcc aaa ggt ccc gcc 528	
Ser Pro Ile Gln Gln Ser Ile Ile Asp Phe Asp Gly Lys Gly Pro Gly	
165 170 175	
cac gag gtc gag atc gcg atg cag tgg aac gcc gcc tac tcg gaa tcc 576	
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	
gtg cac acc ttc gcc aac acc atc aac acc cac gag gcc gcc acc cac 624	
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gaa gag gcc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc 672	
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaa gac aag aag ttg ctg aaa gac aag gac ccg aac ctc acc gcc gac 720	
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225 230 235 240	
gac att cgc gaa gcc ctg gcc gcg gtg atc tcg gtc aag gtc agc gaa 768	
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu	
245 250 255	
ccg cag ttc gag ggt cag acc aag acc aag ctg gcc aac acc gaa gtg 816	
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val	
260 265 270	
aag tcg ttc gtg cag aag gtc tgc aac gaa cag ctc acc cac tgg ttc 864	
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe	
275 280 285	
gag gcc aac ccc gcg gac gcc aag gtg gtg gtc aac aag gcg gtg tcg 912	
Glu Ala Asn Pro Ala Asp Ala Lys Val Val Val Asn Lys Ala Val Ser	
290 295 300	
tcg gcg cag gcc cgg atc gcc gcg cgc aag gcg cga gag ttg gtg cgt 960	
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg	
305 310 315 320	
cgc aag agc gcc acc gat ctg gcc ggg ctg ccc gcc aag ctc gcc gac 1008	
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp	
325 330 335	
tgc cgc tcg acg gat ccg cgc aag tcg gaa ctg tat gtg gtg gag ggt 1056	
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly	
340 345 350	
gat tcg gcc gcc gcc tcg gcg aag agc gcc cgc gac tcg atg ttc cag 1104	
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln	
355 360 365	
gcc atc ctg ccg ctg cgc gcc aag atc atc aac gtc gag aag gcc cgc 1152	
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg	

29
 370 375 380
 atc gac cgg gtg ttg aag aac acc gag gtg cag gcc atc atc acc gcc 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 ctg ggc acc ggc atc cac gac gag ttc gac atc acc aag ctg cgc tat 1248
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 cac aag atc gtg ctg 1263
 His Lys Ile Val Leu
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 1 5 10 15
 gtc tcg gtg gtc aac ggc ctg tcc act cgg ctc gag gtc aac atc gcc 96
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala
 20 25 30
 cgc gac ggc tac gag tgg tcg cag tac tac gac cac gcc gtg ccc ggc 144
 Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
 35 40 45
 acc ctc aag cag ggc gag gcc acc aag cgc acc ggc acc acc atc cgg 192
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
 50 55 60
 ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gaa 240
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 acg gtg gcc cgg cgg ctg cag gaa atg gcg ttc ctc aac aag ggc ctg 288
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 acc atc aac ctc acc gac gag cgg gtg acc aac gaa gag gtc gtc gac 336
 Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
 100 105 110
 gag gtg gtc agc gac acc gcc gac gca ccc aag tcg gcg cag gag aag 384
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
 115 120 125
 gcg gcg gaa tcg gct gcg ccg cat aag gtc aag cac cgc acc ttc cac 432
 Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 tac ccc ggc ggc ctg gtc gac ttc gtc aaa cac atc aat cgc acc aaa 480
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 aac ccc atc cac cag agc atc atc gat ttc ggt ggg aag ggc ccc ggc 528
 Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly

31		32
	165	170
cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg	175	576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser		
	180	185
gtg cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac	190	624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His		
	195	200
gag gag ggc ttc cgc agc gcg ctg acc tcc gtg gtc aac aag tac gcc	205	672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala		
	210	215
aag gac aag aag ctg ctc aag gac aag gac ccc aac ctg acc ggc gac	220	720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp		
	225	230
gac atc cgc gag ggt ttg gcc gcg gtg atc tcg gtc aag gtg agc gaa	235	768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu		
	245	250
ccg cag ttc gag ggc cag acc aag acc aaa ctg ggc aac acc gag gtg	255	816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val		
	260	265
aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc	270	864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe		
	275	280
gaa gcc aac ccc gca gac gcc aaa gtc att gtc aac aag gcg gtt tca	285	912
Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser		
	290	295
tca gcg cag gcg cgc atc gcc gcg cgc aag gcg cga gag ttg gtg cgc	300	960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg		
	305	310
cgc aag agc gca acc gac ctg ggc ggc ctg ccc ggc aag ctc gcc gac	315	1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp		
	325	330
tgc cgg tcg acc gac ccg cgc aag tcg gaa ttg tat gtg gtc gag ggt	335	1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly		
	340	345
gac tcg gcc ggc ggc tcg gcg aaa agc ggc cgg gac tcg atg ttc cag	350	1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln		
	355	360
gcc atc ctt ccg ctg cgc gcc aag atc atc aac gtc gaa aag gcc cgc	365	1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg		
	370	375
atc gac cgg gtg ctg aag aac acc gag gtg cag gcg atc atc acc gcg	380	1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala		
	385	390
ctg ggc acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tac	395	1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr		
	405	410
cac aag atc gtg ttg	415	1263
His Lys Ile Val Leu		
	420	

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 <213> *Mycobacterium gordonae*
 <220>
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Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly	
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gtg tcg gtg gtt aac gcg ttg tcg acg ccg ttg gaa gtc gac atc aaa	96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys	
20 25 30	
cgc gac ggg cac gac tgg tcg cag tat tac aag cgc gcg gtg ccg ggc	144
Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Lys Arg Ala Val Pro Gly	
35 40 45	
acc ctc aag cag ggt gag acg acc cgc aag acc ggc acc aca atc ccg	192
Thr Leu Lys Gln Gly Glu Thr Thr Arg Lys Thr Gly Thr Thr Ile Arg	
50 55 60	
ttc tgg gcg gat ccg gag atc ttc gag acc acc caa tac gac ttc gag	240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu	
65 70 75 80	
acg gtg gcg cgc ccg ctg cag gag atg gcg ttc ctg aac aag ggt ctg	288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acg atc aat ctg acc gac gaa cgc gtc gag cag gac gag gtt gtc gac	336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	
100 105 110	
gag gtc gtc agc gac acc gcc gaa gcg ccc aaa tcc gcc gaa gag aag	384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys	
115 120 125	
gct gcc gaa tcc aag gcc ccg cac aag gtc aag cag cgc acc ttc cac	432
Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys Gln Arg Thr Phe His	
130 135 140	
tat ccc ggt ggt ctg gtc gac ttc gtc aaa cac atc aac cgc acc aaa	480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
agc ccg atc cag cag agc gtc atc gac ttc gaa ggc aaa ggc acc ggc	528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly	
165 170 175	
cac gag gtc gaa atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg	576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	
gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac	624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gaa gag ggc ttc cgc agt gcg ctg acc tcg gtg gtc aac aag tac gcc	672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaa gac aag aag ctg ctc aag gag aag gac ccg aat ctc acc ggt gac	720

35
 Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 gac atc cgg gag ggg ttg gcc gcg gtg atc tcg gtg aag gtc gcc gaa 768
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 ccg cag ttc gag ggt cag acc aag acc aag ctg gcc aac acc gag gtc 816
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc 864
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 gag gcc aat ccg tcg gaa gct aaa acc gtt gtg aac aaa gcg gtg tcg 912
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 tcc gcc cag gcg cgg atc gcc gcg cgc aaa gcg cga gag ctg gtg cgc 960
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 cgc aag agc gca acc gac ctc gcc gcc ctg ccg gcc aag ctc gcc gac 1008
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 tgc cgt tcg acg gat ccc cgc aaa tcc gaa ctg tat gtg gtg gag ggg 1056
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 gac tcc gcc gcc ggc tcg gcc aag agc ggt cgg gat tcg atg ttc cag 1104
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 gcg att ctt ccg ttg cgc gcc aag atc atc aac gtc gag aag gcc cgc 1152
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 atc gac cgg gtg ctg aag aac acc gaa gtc cag gcc atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 ctg gcc acc ggg atc cac gac gag ttc gac atc acc aaa ctg cgc tac 1248
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 cac aag atc gta ttg 1263
 His Lys Ile Val Leu
 420
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 <213> Mycobacterium africanum
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 <222> (1)..(1257)
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 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
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 gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac 96

	37		38
Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp			
20	25	30	
ggg tac gag tgg tct caq gtt tat gag aag tcg gaa ccc ctg ggc ctc			144
Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu			
35	40	45	
aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg			192
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp			
50	55	60	
gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc			240
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val			
65	70	75	80
gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc			288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile			
85	90	95	
aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg			336
Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val			
100	105	110	
gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc			384
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala			
115	120	125	
gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg			432
Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro			
130	135	140	
ggg ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg			480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala			
145	150	155	160
att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag			528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu			
165	170	175	
gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac			576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His			
180	185	190	
acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag			624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu			
195	200	205	
ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac			672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp			
210	215	220	
cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc			720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile			
225	230	235	240
cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag			768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln			
245	250	255	
ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg			816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser			
260	265	270	
ttt gtg cag aag gtc tgt aac gaa cag ctg acc cac tgg ttt gaa gcc			864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala			
275	280	285	

39
 aac ccc acc gac tcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg 912
 Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag 960
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt 1008
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg 1056
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 gcc gcc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata 1104
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 ctt ccg ctg cgc gcc aag atc atc aat gtg gag aaa gcg cgc atc gac 1152
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 ccg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg gcc 1200
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 acc ggg atc cac gac gag ttc gat atc gcc aag ctg cgc tac cac aag 1248
 Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
 405 410 415
 atc gtg ctg 1257
 Ile Val Leu
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 Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 ggg tac gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg gcc ctc 144
 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg 192
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc 240
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc 288

41	Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile	42
	85 90 95	
	aac ctg acc gac gag aag gtg acc caa gac gag gtc gtc gac gaa gtg	336
	Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val	
	100 105 110	
	gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc	384
	Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala	
	115 120 125	
	gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg	432
	Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro	
	130 135 140	
	ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg	480
	Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala	
	145 150 155 160	
	att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag	528
	Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu	
	165 170 175	
	gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac	576
	Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His	
	180 185 190	
	acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag	624
	Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu	
	195 200 205	
	ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac	672
	Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp	
	210 215 220	
	cgc aag cta ctg aag gac aag gac ccc aac ctg acc ggt gac gat atc	720
	Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile	
	225 230 235 240	
	cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag	768
	Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln	
	245 250 255	
	ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg	816
	Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser	
	260 265 270	
	ttt gtg cag aag gtc tgt aac gaa cag ctg acc cac tgg ttt gaa gcc	864
	Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala	
	275 280 285	
	aac ccc acc gac gcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg	912
	Asn Pro Thr Asp Ala Lys Val Val Val Asn Lys Ala Val Ser Ser Ala	
	290 295 300	
	caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag	960
	Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys	
	305 310 315 320	
	agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt	1008
	Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg	
	325 330 335	
	tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg	1056
	Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser	
	340 345 350	

43
 gcc gcc ggt tct gca aaa agc ggt cgc gat tcg atg ttc caq gcq ata 1104
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 ctt ccg ctg cgc gcc aag atc atc aat gtg gag aaa gcg cgc atc gac 1152
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 cgg gtg cta aag aac acc gaa gtt caq gcq atc atc acg gcg ctg gcc 1200
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 acc ggg atc cac gac gag ttc gat atc gcc aag ctg cgc tac cac aag 1248
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 Ile Val Leu
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 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
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 gtg gtc aac gcg ctg tcc atc ccg ctg gag gtg gag atc aag cgc gac 96
 Val Val Asn Ala Leu Ser Ile Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 gcc cat gag tgg tcg caa gtt tat gag aag tcc gag ccg atg gga ctc 144
 Gly His Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Met Gly Leu
 35 40 45
 aag caa gcc gcg ccg acg aag aag acc gcc acg acg gtg cgg ttc tgg 192
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Thr Thr Val Arg Phe Trp
 50 55 60
 gcc gac ccc aac gtt ttt gaa acc acc gag tac gac ttc gaa acc gtc 240
 Ala Asp Pro Asn Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 gcg cga cgg ttg cag gag atg gcg ttt ctc aac aag ggg ctc acc atc 288
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 aac ctg acc gat caq cgg gta acc caq gac gaa gtg gtc gac gag gtg 336
 Asn Leu Thr Asp Gln Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 gtc agc gac gtc gcc gag gcc ccg aag tcg gcc agt gag aag gcg gcc 384
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Lys Ala Ala
 115 120 125
 gaa ttc acc gcc ccc cac aag gtg aag aag cgt acc ttt cac tat ccc 432
 Glu Phe Thr Ala Pro His Lys Val Lys Lys Arg Thr Phe His Tyr Pro
 130 135 140
 ggt gcc ttg gtt gac ttc gtc aag cac atc aac cgc acc aag aac gcc 480

45		46
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala		
145	150	155 160
atc cac agc agc atc gtc gac ttc tcc gga aag ggg acc ggc cac gaa	528	
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu		
165	170	175
gtg gag atc gcg atg cag tgg aat gcc ggc tat tcg gag tcg gtg cac	576	
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His		
180	185	190
acc ttc gcc aac acc atc aac acc cat gag ggc ggg acc cat gaa gaa	624	
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu		
195	200	205
ggg ttc cgc agc gcg ctc acg tcc gtg gtg aac aag tac gcc aag gac	672	
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp		
210	215	220
cgc aaa ctg ctc aaa gac aag gac ccc aac ctc acc ggc gac gac atc	720	
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile		
225	230	235 240
cgg gaa ggg ttg gcc gcg gtg att tcg gtc aaa gtc agc gaa ccg cag	768	
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln		
245	250	255
ttc gag ggc cag acc aag acg aaa cta ggc aac acc gag gtg aag tcg	816	
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser		
260	265	270
ttc gtg cag aag gtg tgc aat gaa cag ctc acc cat tgg ttc gag gcc	864	
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala		
275	280	285
aac ccc gct gat gct aaa acc gtt gtc aac aag gca gtt tca tcg gcg	912	
Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser Ala		
290	295	300
cag gcc agg att gcg gcc cgc aag gcg cgc gag ttg gtg cgc cgc aag	960	
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys		
305	310	315 320
agc gca acc gat ctg ggc gga cta ccg ggc aag ttg gcc gac tgc cgc	1008	
Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg		
325	330	335
tcg acc gac ccc cgt aag tcc gaa tta tat gtg gtg gag ggt gat tca	1056	
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser		
340	345	350
gcc ggc gcc tcg gcg aag agc ggc cgc gac tcg atg ttt caa gcg atc	1104	
Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile		
355	360	365
ttg ccg ttg cgc ggc aag atc atc aac gtc gag aag gcc cgc atc gac	1152	
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp		
370	375	380
cgg gtg ctg aag aac acc gaa gtc cag gcg atc atc acc gcg ttg ggc	1200	
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly		
385	390	395 400
acc ggt att cac gac gaa ttc gac atc gcg aga ctg cgt tac cac aag	1248	

47

48

Thr Gly Ile His Asp Glu Phe Asp Ile Ala Arg Leu Arg Tyr His Lys

405

410

415

atc gtg ctg

1257

Ile Val Leu

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<211> 1263

<212> DNA

<213> Mycobacterium marinum

<220>

<221> CDS

<222> (1)..(1263)

<400> 17

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gtg tcg gtg gtc aac gcg ctg tcc acc cga ctg gaa gtc gac atc aag  96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
      20           25           30
cgc gac gga tac gag tgg tcg cag ttc tac gac cgc gcc cag ccg ggc  144
Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp Arg Ala Gln Pro Gly
      35           40           45
acc ctc aaa cag ggc gag gca acc aag aag acc gga acc acc atc cgg  192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
      50           55           60
ttc tgg gcc gac tcg gac atc ttt gag acc acc gaa tac gac ttc gag  240
Phe Trp Ala Asp Ser Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
      65           70           75           80
acg gtg gcg cgg cgc ctg cag gag atg gcg ttc ctc aac aag ggc ctg  288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
      85           90           95
acc atc aac ctc acc gac gag cgg gtc acc ccg gac gag gtc gtc gac  336
Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Pro Asp Glu Val Val Asp
      100          105          110
gac gtc gtc agt gat acc gcc gaa gca cca aag tcc gcc cag gag aag  384
Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Gln Glu Lys
      115          120          125
gcc gcc gaa tcg acc gcg ccg cac aag gtc aag agc cgc acc ttc cac  432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His
      130          135          140
tat ccc ggc ggt ttg gtc gat ttc gtc aag cac atc aac cgc acc aag  480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
      145          150          155          160
agt ccg att cag cag agc atc gtc gac ttc gag ggc aag ggc tcc gcc  528
Ser Pro Ile Gln Gln Ser Ile Val Asp Phe Glu Gly Lys Gly Ser Gly
      165          170          175
cac gaa gtc gaa atc gcg atg cag tgg aac ggc ggc tac tcg gag tcg  576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
      180          185          190
gtg cac acc ttc gcc aac acc atc aac acc cat gag ggt gga acg cac  624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His

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49
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 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 gac atc cgc gag ggg ttg gcc gcg gtc atc tcg gtg cgg gtg gca gag 768
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Arg Val Ala Glu
 245 250 255
 ccg cag ttc gag ggt cag acg aag acc aag ctg gcc aac acc gag gtc 816
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 aag tcg ttt gtc cag aag gtt tgt aac gag cag ctc acc cac tgg ttc 864
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 275 280 285
 gag gcc aat cct tcg gaa gcc aaa acc att gtg aac aag gcg gta tcc 912
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Ile Val Asn Lys Ala Val Ser
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 Ser Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
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 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
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 370 375 380
 atc gac cga gtc ctg aaa aac act gaa gtc cag gcg atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 ttg ggt acc ggt att cac gac gaa ttc gac ctc tcg aag ctg cgc tat 1248
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Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp	
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Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu	
35 40 45	
aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg 192	
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp	
50 55 60	
gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc 240	
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val	
65 70 75 80	
gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc 288	
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile	
85 90 95	
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Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val	
100 105 110	
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Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala	
115 120 125	
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Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro	
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Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala	
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Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu	
165 170 175	
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Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His	
180 185 190	
acc ttc gcc aac acc atc aac acc cac gag gcc gcc acc cac gaa gag 624	
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu	
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Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp	
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225 230 235 240	
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53

54

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 260 265 270
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 275 280 285
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 290 295 300
 caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cag cgt aag 960
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 305 310 315 320
 agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt 1008
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 325 330 335
 tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg 1056
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 340 345 350
 gcc ggc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata 1104
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac 1152
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg gcc 1200
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag 1248
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 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
 20 25 30
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 Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Glu Arg Ala Val Pro Gly
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 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg

55												56				
50				55				60								
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Phe	Trp	Ala	Asp	Pro	Asp	Ile	Phe	Glu	Thr	Thr	Gln	Tyr	Asp	Phe	Glu	
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Thr	Val	Ala	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu	
85				90				95								
acc	atc	aac	ttg	acc	gac	gag	cgg	gtg	gac	cag	gac	gag	gtc	gtc	gat	336
Thr	Ile	Asn	Leu	Thr	Asp	Glu	Arg	Val	Asp	Gln	Asp	Glu	Val	Val	Asp	
100				105				110								
gaa	gtc	gtc	agc	gac	acc	gcc	gat	gcg	ccc	aaq	tcc	gcc	gaa	gag	aaq	384
Glu	Val	Val	Ser	Asp	Thr	Ala	Asp	Ala	Pro	Lys	Ser	Ala	Glu	Glu	Lys	
115				120				125								
gcg	gcc	gaa	tcc	aaa	gcg	ccg	cac	aaq	gtt	aaq	cac	cgc	acc	ttc	cac	432
Ala	Ala	Glu	Ser	Lys	Ala	Pro	His	Lys	Val	Lys	His	Arg	Thr	Phe	His	
130				135				140								
tac	ccc	ggc	ggc	ttg	gtc	gac	ttc	gtc	aaq	cac	atc	aac	cgg	acc	aaq	480
Tyr	Pro	Gly	Gly	Leu	Val	Asp	Phe	Val	Lys	His	Ile	Asn	Arg	Thr	Lys	
145				150				155				160				
agc	ccg	atc	caa	cag	agc	gtc	atc	gac	ttc	gag	ggc	aaa	ggc	acc	ggc	528
Ser	Pro	Ile	Gln	Gln	Ser	Val	Ile	Asp	Phe	Glu	Gly	Lys	Gly	Thr	Gly	
165				170				175								
cac	gag	gtc	gag	atc	gcg	atg	cag	tgg	aac	ggt	ggc	tac	tcg	gag	tcg	576
His	Glu	Val	Glu	Ile	Ala	Met	Gln	Trp	Asn	Gly	Gly	Tyr	Ser	Glu	Ser	
180				185				190								
gtg	cac	acc	ttc	gcc	aac	acg	atc	aac	acc	cac	gag	ggc	ggt	acg	cac	624
Val	His	Thr	Phe	Ala	Asn	Thr	Ile	Asn	Thr	His	Glu	Gly	Gly	Thr	His	
195				200				205								
gaa	gaa	ggg	ttc	cgc	agt	gcg	ctg	acg	tcg	gtg	gtg	aac	aaa	tac	gcc	672
Glu	Glu	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Ser	Val	Val	Asn	Lys	Tyr	Ala	
210				215				220								
aaa	gac	aaq	aaq	ctg	ctg	aaa	gac	aaq	gac	ccg	aac	ctc	acc	ggt	gac	720
Lys	Asp	Lys	Lys	Leu	Leu	Lys	Asp	Lys	Asp	Pro	Asn	Leu	Thr	Gly	Asp	
225				230				235				240				
gac	atc	cgc	gag	gga	ctg	gcc	gcg	gtg	atc	tcg	gtc	aaq	gtc	gcc	gaa	768
Asp	Ile	Arg	Glu	Gly	Leu	Ala	Ala	Val	Ile	Ser	Val	Lys	Val	Ala	Glu	
245				250				255								
ccc	cag	ttc	gag	ggc	cag	aca	aaq	acc	aaq	ctg	ggc	aac	acc	gag	gtc	816
Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys	Leu	Gly	Asn	Thr	Glu	Val	
260				265				270								
aaq	tcg	ttc	gtg	cag	aaq	gtg	tgc	aac	gaa	cag	ctc	acc	cac	tgg	ttc	864
Lys	Ser	Phe	Val	Gln	Lys	Val	Cys	Asn	Glu</							

57	58
305	320
cgc aag agc gcg acc gat ttg ggc ggg ctg ccc ggc aag ctg gcc gac	1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp	
325	330
tgc cgt tcc acc gac ccg cgc aag tcc gaa ctg tat gtg gtg gag ggt	1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly	
340	345
gac tcg gca ggt ggc tcg gcc aag agc ggc cgt gac tcg atg ttc cag	1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln	
355	360
gcc atc ctg ccg ctg cgc ggc aag atc atc aac gtc gag aag gcc cgc	1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg	
370	380
atc gac cgg gtc ctg aag aac acc gaa gtc cag gcg atc atc acc gcg	1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala	
385	390
ctg ggt acc ggt att cac gac gag ttc gac att tct aaa ctg cgt tac	1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr	
405	410
cac aag atc gtg ttg	415
His Lys Ile Val Leu	1263
420	
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gtg tcg gtg gtc aac gcg ctg tcc acc cgc ctg gag gtc acc atc aag	96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys	
20	25
cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga	144
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly	
35	40
acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg	192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg	
50	55
ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag	240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu	
65	70
acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc	288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85	90
acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac	336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	

59			60
	100	105	110
	gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag	384	
	Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys		
	115	120	125
	gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac	432	
	Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His		
	130	135	140
	tac ccc gcc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag	480	
	Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys		
	145	150	155
	agc ccg atc cag cag agc gtc atc gat ttc gac gcc aag gcc acc gcc	528	
	Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly		
	165	170	175
	cac gag gtc gag atc gcc atg cag tgg aac gcc gcc tac tcg gag tcc	576	
	His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser		
	180	185	190
	gtc cac acc ttc gcc aac acc atc aac acg cac gag gcc gcc acc cac	624	
	Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His		
	195	200	205
	gag gag gcc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc	672	
	Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala		
	210	215	220
	aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac	720	
	Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp		
	225	230	235
	gac atc cgt gag gcc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag	768	
	Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu		
	245	250	255
	cca cag ttc gaa gcc cag acc aag aca aag ctg gcc aac acc gag gtg	816	
	Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val		
	260	265	270
	aag tcg ttc gtg cag aag gtg tgc aac gag cag ctc acc cac tgg ttc	864	
	Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe		
	275	280	285
	gag gcc aac cca tcc gag gcg aaa acg gtg gtg aac aaa gcg gtg tcg	912	
	Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser		
	290	295	300
	tcg gct cag gcg cgc att gcc gcc cgc aag gcg cgt gaa ctg gtg cgc	960	
	Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg		
	305	310	315
	cgc aag agc gcc acc gac ctc gcc ggt ctg ccc gcc aag ctg gcc gac	1008	
	Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp		
	325	330	335
	tgc cgc tcc acc gac ccg ccg aaa tcg gaa ctg tat gtg gtg gag gcc	1056	
	Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly		
	340	345	350
	gat tcg gcc gcc gcc tcg gcc aag agc gcc cgc gac tcg atg ttc cag	1104	
	Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln		
	355	360	365

61
 gcg atc ctg ccg ctg cgc gcc aag atc atc aat gtc gag aag gcc cgc 1152
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380

62
 atc gac cgg gtg ctg aag aac acc gaa gtt cag gcg atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 ctg ggt acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tat 1248
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 cac aag atc gtg ctg 1263
 His Lys Ile Val Leu
 420

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 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Ala
 20 25 30
 acc gac ggg tac gag tgg ttt cag cat tac gac cgc tct gtc ccc gcc 144
 Thr Asp Gly Tyr Glu Trp Phe Gln His Tyr Asp Arg Ser Val Pro Gly
 35 40 45
 acg ctc aag caa gcc gag aaa acc aaa aag acc gcc acc acg gtc cgc 192
 Thr Leu Lys Gln Gly Glu Lys Thr Lys Lys Thr Gly Thr Thr Val Arg
 50 55 60
 ttc tgg gcc gac ccg gac atc ttc gag acg acg gat tac gac ttc gag 240
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Asp Tyr Asp Phe Glu
 65 70 75 80
 acg gtc gca cgc cgg ctg cag gaa atg gcg ttc ctc aac aaa ggg ctg 288
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 acc atc aac ctg acc gac gag cgg gtg cga aac gaa gaa gtc gtc gac 336
 Thr Ile Asn Leu Thr Asp Glu Arg Val Arg Asn Glu Glu Val Val Asp
 100 105 110
 gag gtc gtc agc gac acc gcc gac gcg ccg aag tcg gcg cgc gaa gag 384
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Arg Glu Glu
 115 120 125
 gcc gaa gaa cgg acc acg cag aaa gtc aag cac cgc acg ttc cat tac 432
 Ala Glu Glu Arg Thr Thr Gln Lys Val Lys His Arg Thr Phe His Tyr
 130 135 140

ccc gcc gcc ttg gtc gat ttc gtc aaa cac atc aac cgc aca aag aac 480

63	64
Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn	
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ccc atc cat tcg agc atc gtc gac ttc tcc ggc aag ggt ccc ggc cac	528
Pro Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly His	
165 170 175	
gag gtc gag atc gca atg cag tgg aac gcc ggc tat tcg gag tcg gtg	576
Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val	
180 185 190	
cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa	624
His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu	
195 200 205	
gaa ggc ttc cgc gcg gca ctg acg tcc gtg gtg aac aag tac gcc aag	672
Glu Gly Phe Arg Ala Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys	
210 215 220	
gac cga aaa ctg ctg aag gac aag gac ccc aac ctc acc ggc gac gac	720
Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp	
225 230 235 240	
att cgt gag ggc ctg gcg gcg gtc atc tcg gtc aag gtc agc gag ccg	768
Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro	
245 250 255	
cag ttc gag ggc cag acc aaa acc aaa ctc ggc aac acc gaa gtc aag	816
Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys	
260 265 270	
tcg ttt gtg cag aag gtc tgc aac gaa cag ctc acc cac tgg ttc gag	864
Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu	
275 280 285	
gcc aat ccc agc gac gcc aag acc gtc gtc aac aaa gcg gtg tcg tcg	912
Ala Asn Pro Ser Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser	
290 295 300	
gcg cag gcc cgc att gcc gcc cgc aaa gcg cga gaa ttg gtg cgc cgc	960
Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg	
305 310 315 320	
aag agc gca acc gat ctt gcc ggc ctg ccg ggc aag ctg gct gac tgc	1008
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys	
325 330 335	
cgc tcg acc gat cca cgc aag tcc gaa ttg tat gtg gtg gag ggt gat	1056
Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp	
340 345 350	
tcg gcc ggc ggc tcg gcc aag agc ggc cgc gac tcg atg ttt cag gcg	1104
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala	
355 360 365	
atc ctg ccg ttg cgg gcc aag atc atc aac gtg gag aag gcc cgc atc	1152
Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile	
370 375 380	
gac cgg gtg ctg aag aac act gag gtg cag gcg atc atc acc gcg ctg	1200
Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu	
385 390 395 400	
ggc acc ggc att cac gac gag ttc gac atc tcc aag ctg cgc tac cac	1248
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr His	

65
 405
 410
 415
 66
 1260

aag atc gtg ctg
 Lys Ile Val Leu

420

<210> 22
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 <213> Mycobacterium paratuberculosis
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 gtc tcg gtg gtc aac gcg ctg tcc act cgg ctc gag gtc aac atc gcc 96
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala
 20 25 30
 cgc gac ggc tac gag tgg tcg cag tac tac gac cac gcc gtg ccc ggc 144
 Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
 35 40 45
 acc ctc aag cag ggc gag gcc acc aag cgc acc ggc acc acc atc cgg 192
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
 50 55 60
 ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gaa 240
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 acg gtg gcc cgg cgg ctg cag gaa atg gcg ttc ctc aac aag ggc ctg 288
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 acc atc aac ctc acc gac gag cgg gtg acc aac gaa gag gtc gtc gac 336
 Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
 100 105 110
 gag gtg gtc agc gac acc gcc gac gca ccc aag tcg gcg cag gag aag 384
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
 115 120 125
 gcg gcg gaa tcg gct gcg ccg cat aag gtc aag cac cgc acc ttc cac 432
 Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 tac ccc ggc ggc ctg gtc gac ttc gtc aaa cac atc aat cgc acc aaa 480
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 aac ccc atc cac cag agc atc atc gat ttc ggt ggg aag ggc ccc ggc 528
 Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
 165 170 175
 cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg 576
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 gtg cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac 624
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His

67
195 200 205
gag gag ggc ttc cgc agc gcg ctg acc tcc gtg gtc aac aag tac gcc 672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220
aag gac aag aag ctg ctc aag gac aag gac ccc aac ctg acc ggt gac 720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225 230 235 240
gac atc cgc gag ggt ttg gcc gcg gtg atc tcg gtc aag gtg agc gaa 768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
245 250 255
ccg cag ttc gag ggc cag acc aag acc aaa ctg gcc aac acc gag gtg 816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270
aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc 864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285
gaa gcc aac ccc gca gac gcc aaa gtc att gtc aac aag gcg gtt tca 912
Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
290 295 300
tca gcg cag gcg cgc atc gcc gcg cgc aag gcg cga gag ttg gtg cgc 960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320
cgc aag agc gca acc gac ctg gcc ggg ctg ccc gcc aag ctc gcc gac 1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335
tgc cgg tcg acc gac ccg cgc aag tcg gaa ttg tat gtg gtc gag ggt 1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350
gac tcg gcc ggc ggc tcg gcg aaa agc gcc cgg gac tcg atg ttc cag 1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

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370 375 380
atc gac cgg gtg ctg aag aac acc gag gtg cag gcg atc atc acc gcg 1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400
ctg gcc acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tac 1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415
cac aag atc gtg ttg 1263
His Lys Ile Val Leu
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69
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 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
 115 120 125
 Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala

71
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 405 410 415
 His Lys Ile Val Leu
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 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
 115 120 125
 Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
 130 135 140
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
 195 200 205
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
 245 250 255
 Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
 260 265 270
 Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
 275 280 285
 Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300

73

74

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
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 Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
 405 410 415
 Ile Val Leu
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 <213> Mycobacterium szulgai
 <400> 25
 Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
 20 25 30
 Arg Asp Gly His Lys Trp Ser Gln Phe Tyr Asn Lys Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Ala Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
 115 120 125
 Ala Ala Glu Ser Lys Gly Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Ile Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Ser Pro Ile Gln Gln Ser Val Val Ala Phe Asp Gly Lys Gly Glu Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Ala Asn Leu Thr Gly Asp
 225 230 235 240

75
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ala Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
 420

<210> 26

<211> 421

<212> PRT

<213> *Mycobacterium malmoeense*

<400> 26

Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Val Ala
 20 25 30
 Arg Asp Gly Tyr Met Trp Ser Gln Phe Tyr Asp His Ala Glu Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Thr Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Glu Glu Glu Val Val Asp
 100 105 110
 Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Val Glu Lys
 115 120 125
 Ala Ala Glu Ser Thr Gly Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Asn Pro Ile His Asn Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly

165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
 420

<210> 27

<211> 421

<212> PRT

<213> Mycobacterium intracellulare

<400> 27

Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Ala
 20 25 30
 Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp His Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95

79
 Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Asn Glu Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
 115 120 125
 Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Ser Pro Ile Gln Gln Ser Ile Ile Asp Phe Asp Gly Lys Gly Pro Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ala Asp Ala Lys Val Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
 420
 <210> 28
 <211> 421
 <212> PRT
 <213> Mycobacterium avium
 <400> 28
 Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala

81
 20 25 30
 Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
 115 120 125
 Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu

420

<210> 29

<211> 421

<212> PRT

<213> *Mycobacterium goodnae*

<400> 29

Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
 20 25 30

Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Lys Arg Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Thr Thr Arg Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
 115 120 125
 Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys Gln Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335

85

86

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
 420
 <210> 30
 <211> 419
 <212> PRT
 <213> Mycobacterium africanum
 <400> 30
 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1 5 10 15
 Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
 115 120 125
 Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
 130 135 140
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
 195 200 205
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
 245 250 255
 Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser

260 265 270
 Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
 275 280 285
 Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
 405 410 415
 Ile Val Leu
 <210> 31
 <211> 419
 <212> PRT
 <213> Mycobacterium tuberculosis
 <400> 31
 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1 5 10 15
 Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
 115 120 125
 Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
 130 135 140
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu

89

90

195 200 205
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
 245 250 255
 Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
 260 265 270
 Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
 275 280 285
 Asn Pro Thr Asp Ala Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
 405 410 415
 Ile Val Leu
 <210> 32
 <211> 419
 <212> PRT
 <213> Mycobacterium gastri
 <400> 32
 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1 5 10 15
 Val Val Asn Ala Leu Ser Ile Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 Gly His Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Met Gly Leu
 35 40 45
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Thr Thr Val Arg Phe Trp
 50 55 60
 Ala Asp Pro Asn Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 Asn Leu Thr Asp Gln Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Lys Ala Ala
 115 120 125
 Glu Phe Thr Ala Pro His Lys Val Lys Lys Arg Thr Phe His Tyr Pro

91

92

130 135 140
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
 195 200 205
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
 245 250 255
 Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
 260 265 270
 Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
 275 280 285
 Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400
 Thr Gly Ile His Asp Glu Phe Asp Ile Ala Arg Leu Arg Tyr His Lys
 405 410 415

Ile Val Leu

<210> 33

<211> 421

<212> PRT

<213> Mycobacterium marinum

<400> 33

Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
 20 25 30
 Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp Arg Ala Gln Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Ser Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu

93 65 70 75 80 94
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Pro Asp Glu Val Val Asp
 100 105 110
 Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Gln Glu Lys
 115 120 125
 Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Ser Pro Ile Gln Gln Ser Ile Val Asp Phe Glu Gly Lys Gly Ser Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Arg Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Ile Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ser Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
 420

<210> 34

<211> 419

<212> PRT

<213> Mycobacterium microti

<400> 34

95
 Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1 5 10 15
 Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
 20 25 30
 Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
 35 40 45
 Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
 50 55 60
 Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65 70 75 80
 Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
 85 90 95
 Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
 100 105 110
 Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
 115 120 125
 Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
 130 135 140
 Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
 145 150 155 160
 Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
 165 170 175
 Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
 180 185 190
 Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
 195 200 205
 Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
 210 215 220
 Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
 225 230 235 240
 Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
 245 250 255
 Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
 260 265 270
 Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
 275 280 285
 Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
 290 295 300
 Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
 305 310 315 320
 Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
 325 330 335
 Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
 340 345 350
 Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
 355 360 365
 Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
 370 375 380
 Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
 385 390 395 400

97

98

Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
 405 410 415
 Ile Val Leu
 <210> 35
 <211> 421
 <212> PRT
 <213> *Mycobacterium asiaticum*
 <400> 35
 Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
 20 25 30
 Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Glu Arg Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Asp Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Glu Glu Lys
 115 120 125
 Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335

99

100

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
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 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
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 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
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 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
 115 120 125
 Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
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 145 150 155 160
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 225 230 235 240
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 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val

101

102

260 265 270
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 Thr Leu Lys Gln Gly Glu Lys Thr Lys Lys Thr Gly Thr Thr Val Arg
 50 55 60
 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Asp Tyr Asp Phe Glu
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 Thr Ile Asn Leu Thr Asp Glu Arg Val Arg Asn Glu Glu Val Val Asp
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 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Arg Glu Glu
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 Ala Glu Glu Arg Thr Thr Gln Lys Val Lys His Arg Thr Phe His Tyr
 130 135 140
 Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn
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 Pro Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly His
 165 170 175
 Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val
 180 185 190

103
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 210 215 220
 Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp
 225 230 235 240
 Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro
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 260 265 270
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 Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
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 355 360 365
 Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile
 370 375 380
 Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu
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 Lys Ile Val Leu
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<213> Mycobacterium paratuberculosis

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 Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
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 Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys

105
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 Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
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 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
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 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
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 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
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 405 410 415
 His Lys Ile Val Leu

420

<210> 39

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<400> 39

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【図面の簡単な説明】

【図1】 マイコバクテリウム・カンサシイとマイコバクテリウム・ガストリのgyrB遺伝子の塩基配列を示す図。

【図2】 配列番号1、3、5により表されるプライマー*

*を用いたPCRの結果を示す図。

【図3】 分子系統解析により作製された遅発育性マイコバクテリアの系統樹を示す図。

【図1】

```

MKAN 1: TCGACGCGCTACCGATATCGCGCGGCTGACGGTGTGCTCTCTGCTGTCACGCA 60
MGAS 1: .....T.....T.A.....G 60
      CCGCGCGCGGCTACCGATATCGCGCGGCTGACGGTGTGCTCTCTGCTGTCACGCA

MKAN 61: CTCTGACCGCGCTGACGCTGACATCAGCGCGCGGCTGACGCTGCTGCTGCTTAC 120
MGAS 61: .....T.....A.....T 120
      CCGCGCGCGGCTGACGCTGACATCAGCGCGGCTGACGCTGCTGCTGCTTAC

MKAN 121: GAGAAATCGACGCGATGCGACTCAGCAGCGCGCGGCTGACGAGCGCGCGGCG 180
MGAS 121: .....G.....G..... 180
      CCGCGCGCGGCTGACGCGATGCGACTCAGCAGCGCGGCTGACGAGCGCGCGGCG

MKAN 181: GTGCGCTTCTGCGCGGCTGCGCAATGCTTTTTCAGCGCGGCTGACGCTGCGAACTG 240
MGAS 181: .....C.....A..... 240
      CCGCGCGCGGCTGCGCAATGCTTTTTCAGCGCGGCTGACGCTGCGAACTG

MKAN 241: GCACGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 300
MGAS 241: .....G.....C..... 300
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 301: CACCGCGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 360
MGAS 301: .....A.....A.....G 360
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 361: AAGTGGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 420
MGAS 361: .....T.A.....C.....E..... 420
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 421: TTGCGCTTCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
MGAS 421: .....T.....CT.....C..... 479
      CCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

MKAN 480: CAGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 538
MGAS 480: .....A.....CA..... 538
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 539: CGACGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 598
MGAS 539: .....C..... 598
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 599: CCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 658
MGAS 599: .....T.....T.....A.....C.....G.....C..... 658
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 659: AGTGGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 718
MGAS 659: .....A.....C..... 718
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 719: TCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 778
MGAS 719: .....A.....A..... 778
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 779: AGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 838
MGAS 779: .....A.....T..... 838
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 839: AACCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 898
MGAS 839: .....T..... 898
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 899: CGCTTTCAGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 957
MGAS 899: .....A.....G.....CA.....E..... 957
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 958: AAGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 1017
MGAS 958: .....G.....T.....G..... 1017
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 1018: CCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 1077
MGAS 1018: .....C.....T.....A..... 1077
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 1078: GGTGGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 1137
MGAS 1078: .....C.....T.....A.....C..... 1137
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 1138: AAGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 1197
MGAS 1138: ..... 1197
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

MKAN 1198: GGTGGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG 1257
MGAS 1198: .....C.....T.....T.....G..... 1257
      CCGCGCGCGGCTGCGGAGCTGCGCTTTCAGCGCGGCTGCGCAATGCTGCGAACTG

```

図1: Mycobacterium kansasii(上段)とMycobacterium goodii(下段)のgyrB配列の比較。同一の塩基配列の部分は黒印で示し、Mycobacterium kansasiiの配列のみを示した。

【図2】

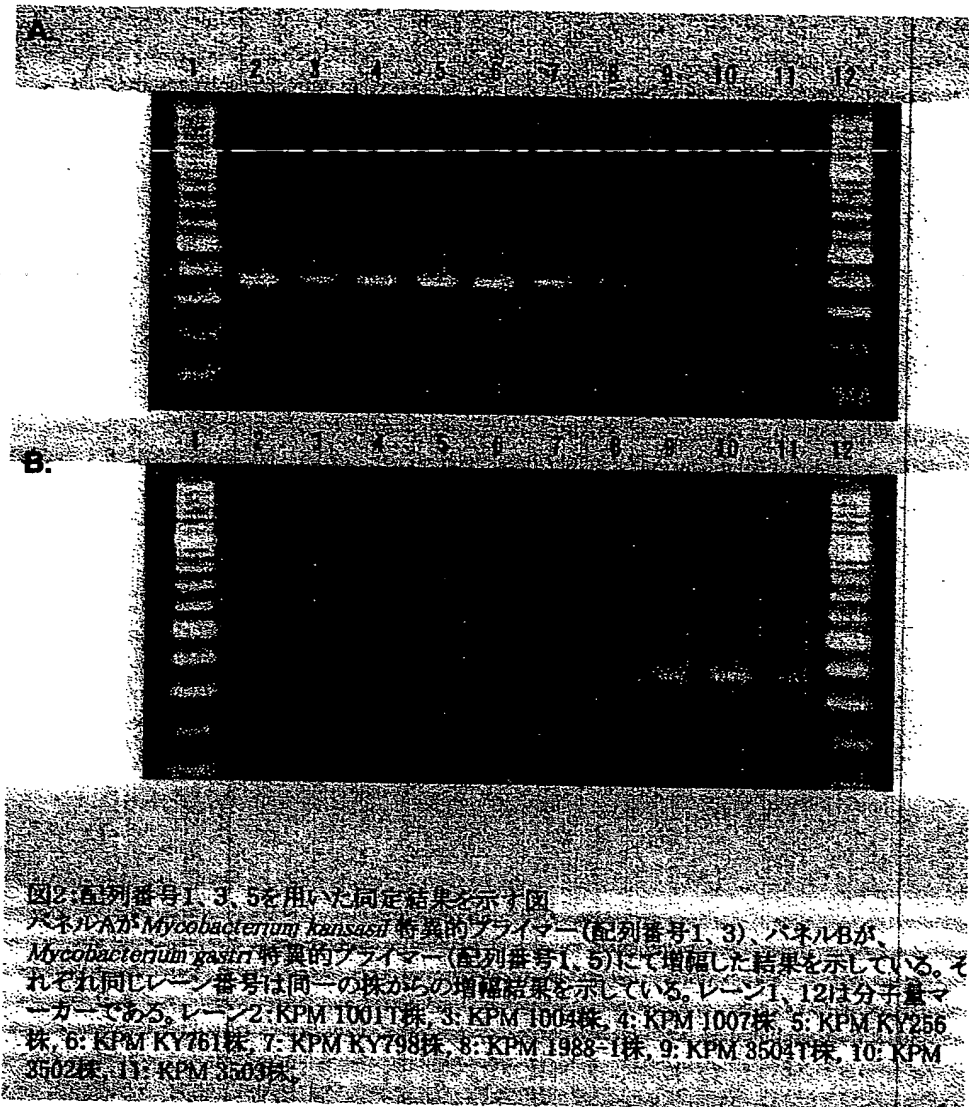


図2: 配列番号1, 3, 5を用いた同定結果を示す図

パネルAが *Mycobacterium kansasii* 特異的プライマー (配列番号1, 3)、パネルBが *Mycobacterium gastri* 特異的プライマー (配列番号1, 5) にて増幅した結果を示している。それぞれ同じレーン番号は同一の株からの増幅結果を示している。レーン1, 12は分子重量マーカーである。レーン2: KPM 1001株, 3: KPM 1004株, 4: KPM 1007株, 5: KPM KY256株, 6: KPM KY761株, 7: KPM KY798株, 8: KPM 1988-1株, 9: KPM 35041株, 10: KPM 3502株, 11: KPM 3503株。

【図3】

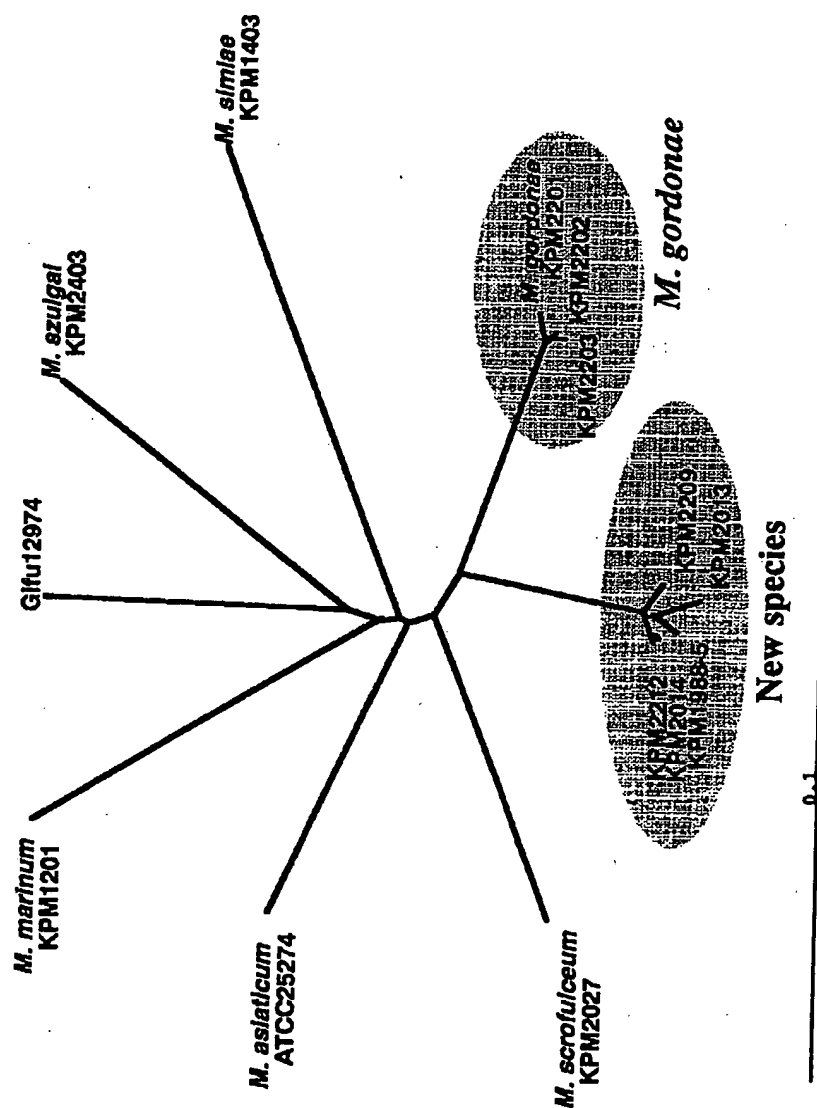


図3: gyrB配列の解析から新しい種の運育性マイコンバクテリアの存在が示された例
分子系統解析を行い、得られたgyrB配列と既に調べられているgyrB配列を比較することにより、KPM 2212, 2014, 1988-5, 2209, 2013の一群の株が新規の種であることが示された。

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社海洋バイオテクノロジー研究所釜石研
究所内

Fターム(参考) 4B024 AA11 CA09 DA05 HA19
4B063 QA01 QQ06 QQ42 QR32 QR55
QR62 QS25

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The 16s/23s ribosomal spacer region as a target for DNA probes to identify eubacteria.

Barry T, Colleran G, Glennon M, Dunican LK, Gannon F.

National Diagnostic Centre, BioResearch Ireland, University College Galway.

Variable regions of the 16s ribosomal RNA have been frequently used as the target for DNA probes to identify microorganisms. In some situations, however, there is very little sequence variation observed between the 16s rRNA genes of closely related microorganisms. This study presents a general method to obtain species-specific probes using the spacer (intergenic) region between the 16s and 23s rRNA genes. The overall strategy is analogous to that which has previously been developed for the variable regions of the 16s rRNA genes. Sequence analysis of the 16s rRNA and 23s rRNA coding sequences flanking the spacer regions resulted in the design of PCR primers that can be used to amplify the spacer regions of a wide range of eubacteria. Sequencing the amplified spacer region then gives rise to the information that can be used to select specific DNA sequences for use as a DNA probe or for the generation of specific PCR primers to a microorganism of interest. In this study the approach to develop specific DNA markers for members of the genus *Clostridium* is described in detail. A specific DNA oligonucleotide probe and PCR primers have been designed for *Clostridium perfringens* that distinguish it from other organisms in the genus.

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